



It will be in the hands of the people.

03060501 070000

405										410					415				
Lys	Ser	Ile	Pro	Leu	Arg	Arg	Gln	Val	Thr	Val	Ser	Ala	Asp	Ser	Ser				
			420					425					430						
Ala	Ser	Met	Asn	Ser	Gly	Val	Leu	Leu	Val	Arg	Pro	Ser	Arg	Leu	Ser				
		435					440					445							
Ser	Ser	Gly	Thr	Pro	Met	Leu	Ala	Gly	Val	Ser	Glu	Tyr	Glu	Leu	Pro				
		450				455					460								
Glu	Asp	Pro	Arg	Trp	Glu	Leu	Pro	Arg	Asp	Arg	Leu	Val	Leu	Gly	Lys				
465					470				475						480				
Pro	Leu	Gly	Glu	Gly	Cys	Phe	Gly	Gln	Val	Val	Leu	Ala	Glu	Ala	Ile				
				485				490						495					
Gly	Leu	Asp	Lys	Asp	Lys	Pro	Asn	Arg	Val	Thr	Lys	Val	Ala	Val	Lys				
			500					505					510						
Met	Leu	Lys	Ser	Asp	Ala	Thr	Glu	Lys	Asp	Leu	Ser	Asp	Leu	Ile	Ser				
		515					520					525							
Glu	Met	Glu	Met	Met	Lys	Met	Ile	Gly	Lys	His	Lys	Asn	Ile	Ile	Asn				
		530				535					540								
Leu	Leu	Gly	Ala	Cys	Thr	Gln	Asp	Gly	Pro	Leu	Tyr	Val	Ile	Val	Glu				
545					550				555						560				
Tyr	Ala	Ser	Lys	Gly	Asn	Leu	Arg	Glu	Tyr	Leu	Gln	Ala	Arg	Arg	Pro				
			565					570						575					
Pro	Gly	Leu	Glu	Tyr	Cys	Tyr	Asn	Pro	Ser	His	Asn	Pro	Glu	Glu	Gln				
			580					585					590						
Leu	Ser	Ser	Lys	Asp	Leu	Val	Ser	Cys	Ala	Tyr	Gln	Val	Ala	Arg	Gly				
		595					600					605							
Met	Glu	Tyr	Leu	Ala	Ser	Lys	Lys	Cys	Ile	His	Arg	Asp	Leu	Ala	Ala				
		610				615					620								
Arg	Asn	Val	Leu	Val	Thr	Glu	Asp	Asn	Val	Met	Lys	Ile	Ala	Asp	Phe				
625					630				635						640				
Gly	Leu	Ala	Arg	Asp	Ile	His	His	Ile	Asp	Tyr	Tyr	Lys	Lys	Thr	Thr				
			645					650						655					
Asn	Gly	Arg	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ala	Leu	Phe	Asp				
			660					665					670						
Arg	Ile	Tyr	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Leu	Leu				
		675					680					685							
Trp	Glu	Ile	Phe	Thr	Leu	Gly	Gly	Ser	Pro	Tyr	Pro	Gly	Val	Pro	Val				
		690				695					700								
Glu	Glu	Leu	Phe	Lys	Leu	Leu	Lys	Glu	Gly	His	Arg	Met	Asp	Lys	Pro				
705					710				715					720					
Ser	Asn	Cys	Thr	Asn	Glu	Leu	Tyr	Met	Met	Met	Arg	Asp	Cys	Trp	His				
			725					730						735					
Ala	Val	Pro	Ser	Gln	Arg	Pro	Thr	Phe	Lys	Gln	Leu	Val	Glu	Asp	Leu				
			740					745					750						
Asp	Arg	Ile	Val	Ala	Leu	Thr	Ser	Asn	Gln	Glu	Tyr	Leu	Asp	Leu	Ser				
		755					760					765							

Met Pro Leu Asp Gln Tyr Ser Pro Ser Phe Pro Asp Thr Arg Ser Ser  
770 775 780

Thr Cys Ser Ser Gly Glu Asp Ser Val Phe Ser His Glu Pro Leu Pro  
785 790 795 800

Glu Glu Pro Cys Leu Pro Arg His Pro Ala Gln Leu Ala Asn Gly Gly  
805 810 815

Leu Lys Arg Arg  
820

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Trp Ser Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala  
1 5 10 15  
Thr Leu Cys Thr Ala Arg Pro Ser Pro Thr Leu Pro Glu Gln Ala Gln  
20 25 30  
Pro Trp Gly Ala Pro Val Glu Val Glu Ser Phe Leu Val His Pro Gly  
35 40 45  
Asp Leu Leu Gln Leu Arg Cys Arg Leu Arg Asp Asp Val Gln Ser Ile  
50 55 60  
Asn Trp Leu Arg Asp Gly Val Gln Leu Ala Glu Ser Asn Arg Thr Arg  
65 70 75 80  
Ile Thr Gly Glu Glu Val Glu Val Gln Asp Ser Val Pro Ala Asp Ser  
85 90 95  
Gly Leu Tyr Ala Cys Val Thr Ser Ser Pro Ser Gly Ser Asp Thr Thr  
100 105 110  
Tyr Phe Ser Val Asn Val Ser Asp Ala Leu Pro Ser Ser Glu Asp Asp  
115 120 125  
Asp Asp Asp Asp Asp Ser Ser Ser Glu Glu Lys Glu Thr Asp Asn Thr  
130 135 140  
Lys Pro Asn Arg Met Pro Val Ala Pro Tyr Trp Thr Ser Pro Glu Lys  
145 150 155 160  
Met Glu Lys Lys Leu His Ala Val Pro Ala Ala Lys Thr Val Lys Phe  
165 170 175  
Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr Leu Arg Trp Leu Lys  
180 185 190  
Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile Gly Gly Tyr Lys Val  
195 200 205

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09060561.073000

Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser Val Val Pro Ser Asp  
210 215 220

Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu Tyr Gly Ser Ile Asn  
225 230 235 240

His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser Pro His Arg Pro Ile  
245 250 255

Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val Ala Leu Gly Ser Asn  
260 265 270

Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro Gln Pro His Ile Gln  
275 280 285

Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys Ile Gly Pro Asp Asn  
290 295 300

Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly Val Asn Thr Thr Asp  
305 310 315 320

Lys Glu Met Glu Val Leu His Leu Arg Asn Val Ser Phe Glu Asp Ala  
325 330 335

Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile Gly Leu Ser His His  
340 345 350

Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu Glu Arg Pro Ala Val  
355 360 365

Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile Tyr Cys Thr Gly Ala  
370 375 380

Phe Leu Ile Ser Cys Met Val Gly Ser Val Ile Val Tyr Lys Met Lys  
385 390 395 400

Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln Met Ala Val His Lys  
405 410 415

Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val Thr Val Ser Ala Asp  
420 425 430

Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu Val Arg Pro Ser Arg  
435 440 445

Leu Ser Ser Ser Gly Thr Pro Met Leu Ala Gly Val Ser Glu Tyr Glu  
450 455 460

Leu Pro Glu Asp Pro Arg Trp Glu Leu Pro Arg Asp Arg Leu Val Leu  
465 470 475 480

Gly Lys Pro Leu Gly Glu Gly Cys Phe Gly Gln Val Val Leu Ala Glu  
485 490 495

Ala Ile Gly Leu Asp Lys Asp Lys Pro Asn Arg Val Thr Lys Val Ala  
500 505 510

Val Lys Met Leu Lys Ser Asp Ala Thr Glu Lys Asp Leu Ser Asp Leu  
515 520 525

Ile Ser Glu Met Glu Met Met Lys Met Ile Gly Lys His Lys Asn Ile  
530 535 540

Ile Asn Leu Leu Gly Ala Cys Thr Gln Asp Gly Pro Leu Tyr Val Ile  
545 550 555 560

Val Glu Tyr Ala Ser Lys Gly Asn Leu Arg Glu Tyr Leu Gln Ala Arg

565										570					575						
Arg	Pro	Pro	Gly	Leu	Glu	Tyr	Cys	Tyr	Asn	Pro	Ser	His	Asn	Pro	Glu						
			580					585					590								
Glu	Gln	Leu	Ser	Ser	Lys	Asp	Leu	Val	Ser	Cys	Ala	Tyr	Gln	Val	Ala						
		595					600					605									
Arg	Gly	Met	Glu	Tyr	Leu	Ala	Ser	Lys	Lys	Cys	Ile	His	Arg	Asp	Leu						
	610					615					620										
Ala	Ala	Arg	Asn	Val	Leu	Val	Thr	Glu	Asp	Asn	Val	Met	Lys	Ile	Ala						
625					630					635					640						
Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	His	His	Ile	Asp	Tyr	Tyr	Lys	Lys						
				645					650					655							
Thr	Thr	Asn	Gly	Arg	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ala	Leu						
			660					665					670								
Phe	Asp	Arg	Ile	Tyr	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val						
		675					680					685									
Leu	Leu	Trp	Glu	Ile	Phe	Thr	Leu	Gly	Gly	Ser	Pro	Tyr	Pro	Gly	Val						
	690					695					700										
Pro	Val	Glu	Glu	Leu	Phe	Lys	Leu	Leu	Lys	Glu	Gly	His	Arg	Met	Asp						
705					710					715					720						
Lys	Pro	Ser	Asn	Cys	Thr	Asn	Glu	Leu	Tyr	Met	Met	Met	Arg	Asp	Cys						
			725						730					735							
Trp	His	Ala	Val	Pro	Ser	Gln	Arg	Pro	Thr	Phe	Lys	Gln	Leu	Val	Glu						
			740					745						750							
Asp	Leu	Asp	Arg	Ile	Val	Ala	Leu	Thr	Ser	Asn	Gln	Glu	Tyr	Leu	Asp						
	755						760					765									
Leu	Ser	Met	Pro	Leu	Asp	Gln	Tyr	Ser	Pro	Ser	Phe	Pro	Asp	Thr	Arg						
	770					775					780										
Ser	Ser	Thr	Cys	Ser	Ser	Gly	Glu	Asp	Ser	Val	Phe	Ser	His	Glu	Pro						
785					790					795					800						
Leu	Pro	Glu	Glu	Pro	Cys	Leu	Pro	Arg	His	Pro	Ala	Gln	Leu	Ala	Asn						
				805					810					815							
Arg	Gly	Leu	Lys	Arg	Arg																
			820																		

(i) SEQUENCE/CHARACTERISTICS:

- (A) LENGTH: 731 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

/(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Trp Ser Trp Lys Cys Leu Leu Phe Trp Ala Val Leu Val Thr Ala  
1 5 10 15

Thr Leu Cys Thr Ala Arg Pro Ser Pro Thr Leu Pro Glu Gln Asp Ala  
 20 25 30  
 Leu Pro Ser Ser Glu Asp Asp Asp Asp Asp Ser Ser Ser Glu  
 35 40 45  
 Glu Lys Glu Thr Asp Asn Thr Lys Pro Asn Pro Val Ala Pro Tyr Trp  
 50 55 60  
 Thr Ser Pro Glu Lys Met Glu Lys Lys Leu His Ala Val Pro Ala Ala  
 65 70 75 80  
 Lys Thr Val Lys Phe Lys Cys Pro Ser Ser Gly Thr Pro Asn Pro Thr  
 85 90 95  
 Leu Arg Trp Leu Glu Asn Gly Lys Glu Phe Lys Pro Asp His Arg Ile  
 100 105 110  
 Gly Gly Tyr Lys Val Arg Tyr Ala Thr Trp Ser Ile Ile Met Asp Ser  
 115 120 125  
 Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys Ile Val Glu Asn Glu  
 130 135 140  
 Tyr Gly Ser Ile Asn His Thr Tyr Gln Leu Asp Val Val Glu Arg Ser  
 145 150 155 160  
 Pro His Arg Pro Ile Leu Gln Ala Gly Leu Pro Ala Asn Lys Thr Val  
 165 170 175  
 Ala Leu Gly Ser Asn Val Glu Phe Met Cys Lys Val Tyr Ser Asp Pro  
 180 185 190  
 Gln Pro His Ile Gln Trp Leu Lys His Ile Glu Val Asn Gly Ser Lys  
 195 200 205  
 Ile Gly Pro Asp Asn Leu Pro Tyr Val Gln Ile Leu Lys Thr Ala Gly  
 210 215 220  
 Val Asn Thr Thr Asp Lys Glu Met Glu Val Leu His Leu Arg Asn Val  
 225 230 235 240  
 Ser Phe Glu Asp Ala Gly Glu Tyr Thr Cys Leu Ala Gly Asn Ser Ile  
 245 250 255  
 Gly Leu Ser His His Ser Ala Trp Leu Thr Val Leu Glu Ala Leu Glu  
 260 265 270  
 Glu Arg Pro Ala Val Met Thr Ser Pro Leu Tyr Leu Glu Ile Ile Ile  
 275 280 285  
 Tyr Cys Thr Gly Ala Phe Leu Ile Ser Cys Met Val Gly Ser Val Ile  
 290 295 300  
 Val Tyr Lys Met Lys Ser Gly Thr Lys Lys Ser Asp Phe His Ser Gln  
 305 310 315 320  
 Met Ala Val His Lys Leu Ala Lys Ser Ile Pro Leu Arg Arg Gln Val  
 325 330 335  
 Thr Val Ser Ala Asp Ser Ser Ala Ser Met Asn Ser Gly Val Leu Leu  
 340 345 350  
 Val Arg Pro Ser Arg Leu Ser Ser Ser Gly Thr Pro Met Leu Ala Gly  
 355 360 365

05660361 070000

[illegible]

Ala Gln Leu Ala Asn Gly Gly Leu Lys Arg Arg



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Trp	Ser	Trp	Lys	Cys	Leu	Leu	Phe	Trp	Ala	Val	Leu	Val	Thr	Ala
1				5					10					15	
Thr	Leu	Cys	Thr	Ala	Arg	Pro	Ser	Pro	Thr	Leu	Pro	Glu	Gln	Asp	Ala
			20					25					30		
Leu	Pro	Ser	Ser	Glu	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Ser	Ser	Ser	Glu
		35					40					45			
Glu	Lys	Glu	Thr	Asp	Asn	Thr	Lys	Pro	Asn	Arg	Met	Pro	Val	Ala	Pro
	50					55					60				
Tyr	Trp	Thr	Ser	Pro	Glu	Lys	Met	Glu	Lys	Lys	Leu	His	Ala	Val	Pro
65					70					75					80
Ala	Ala	Lys	Thr	Val	Lys	Phe	Lys	Cys	Pro	Ser	Ser	Gly	Thr	Pro	Asn
				85					90					95	
Pro	Thr	Leu	Arg	Trp	Leu	Lys	Asn	Gly	Lys	Glu	Phe	Lys	Pro	Asp	His
			100					105					110		
Arg	Ile	Gly	Gly	Tyr	Lys	Val	Arg	Tyr	Ala	Thr	Trp	Ser	Ile	Ile	Met
		115					120						125		
Asp	Ser	Val	Val	Pro	Ser	Asp	Lys	Gly	Asn	Tyr	Thr	Cys	Ile	Val	Glu
		130				135					140				
Asn	Glu	Tyr	Gly	Ser	Ile	Asn	His	Thr	Tyr	Gln	Leu	Asp	Val	Val	Glu
145					150					155					160
Arg	Ser	Pro	His	Arg	Pro	Ile	Leu	Gln	Ala	Gly	Leu	Pro	Ala	Asn	Lys
				165					170					175	
Thr	Val	Ala	Leu	Gly	Ser	Asn	Val	Glu	Phe	Met	Cys	Lys	Val	Tyr	Ser
			180					185					190		
Asp	Pro	Gln	Pro	His	Ile	Gln	Trp	Leu	Lys	His	Ile	Glu	Val	Asn	Gly
		195					200					205			
Ser	Lys	Ile	Gly	Pro	Asp	Asn	Leu	Pro	Tyr	Val	Gln	Ile	Leu	Lys	Thr
	210					215					220				
Ala	Gly	Val	Asn	Thr	Thr	Asp	Lys	Glu	Met	Glu	Val	Leu	His	Leu	Arg
225					230					235					240
Asn	Val	Ser	Phe	Glu	Asp	Ala	Gly	Glu	Tyr	Thr	Cys	Leu	Ala	Gly	Asn
				245					250					255	
Ser	Ile	Gly	Leu	Ser	His	His	Ser	Ala	Trp	Leu	Thr	Val	Leu	Glu	Ala
			260					265					270		



(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 300 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: ~~SEQ~~ ID NO:5:

# 25th Anniversary

175

Glu Gln Arg Ala Ala Gly Met Gly Gly Ala Gly Leu  
290 295 300

Asp Ser Val Val Pro Ser Asp Lys Gly Asn Tyr Thr Cys Ile Val Glu  
130 135 140

**THE**

Ser Trp Glu Gln Arg Ala Ala Gly Met Gly Gly Ala Gly Leu  
290 295 300

## 30

[illegible]

It is not enough to say that the world is a place of suffering and that we must do something to help. We must also ask ourselves why the world is a place of suffering. Is it because of the way we live? Is it because of the way we think? Is it because of the way we feel? The answer is yes to all of these questions. The world is a place of suffering because of the way we live, the way we think, and the way we feel. We must change the way we live, the way we think, and the way we feel if we want to make the world a better place.

(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "Synthetic"
```

CCAACCTCTA GAGGATCCAC TGGGATGTGG AGCTGGAAGT GC

42

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 42 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "Synthetic"
```

GTAAGCGGCC GCGGATCCTT ACTACTCCAG GTACAGGGGC GA

42

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: /other nucleic acid  
(A) DESCRIPTION: /desc = "Synthetic"

CCATTGGAT CCGT/CACAGC CACACTCTGC ACCGCT

36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: other nucleic acid
      (A) DESCRIPTION: /desc = "Synthetic"
```

Ant 30

i) SEQUENCE DESCRIPTION: SEQ ID NO:12:  
GTCTG ACTTCCATCT TTTCTGGGGA TGTCCA

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